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RAPIDLY GROWING HIV TRANSMISSION CLUSTERS IN THE UNITED STATES, 2013–2016

Epidemiology/Public Health: (R) Epidemiology

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Background: In early 2016, CDC began routinely analyzing molecular sequence data reported to the National HIV Surveillance System (NHSS) to identify transmission clusters suggestive of recent and rapid growth in the United States. An assessment of the initial 13 clusters identified demonstrated transmission rates greater than the 4/100 person-years (py) estimated for the entire United States. Here, we assessed transmission rates, characteristics, and geographic distribution of all rapidly growing clusters identified during the first 15 months of implementation.

Methods: At quarterly intervals during December 31, 2015– December 31, 2016, we analyzed partial HIV-1 pol sequences reported to the NHSS for persons with HIV diagnosed during the 3 years prior. We calculated genetic distance for each pair of sequences and inferred clusters using a pairwise threshold of 0.005 substitutions/site. Rapidly growing clusters were defined as those with ≥ 5 diagnoses during the most recent 12-month period. We used node ages inferred by molecular clock phylogenetic analysis to estimate HIV transmission rates for these clusters and compared demographic characteristics and transmission category of persons in these clusters to other persons with HIV diagnosed during January 1, 2013 – December 31, 2016 who had sequences available. The Rao-Scott correction to the Pearson Chi-Square test was used to account for correlation between cases in the same cluster.

Results: Among 51,750 persons with sequences analyzed, 60 rapidly growing transmission clusters were identified. Rapidly growing clusters were 5–42 persons in size, with transmission rates ranging from 21–132 transmission events/100 py (median: 44 per 100 py). Compared with the 50,847 persons not in rapidly growing clusters, the 903 persons in rapidly growing clusters were disproportionately young men who have sex with men (MSM) (61% vs 32% $p < .0001$), and particularly young Hispanic/Latino MSM (26% vs 10%, $p < .0001$). Clusters were identified in all regions of the country and involved 20 states.

Conclusion: Routine surveillance for rapidly growing clusters consistently identifies clusters across the United States with transmission rates far exceeding the estimated national rate. These findings suggest rapid transmission in networks involving young MSM, especially young Hispanic MSM. Prioritizing these clusters for public health intervention may have increased potential to reduce future infections.